

SEQUENCE LISTING

<110> Russell, William
Klaenhammer, Todd

<120> LACTOBACILLUS BETA-GLUCURONIDASE AND DNA ENCODING THE SAME

<130> 5051.514

<150> 60/206,372
<151> 2000-05-23

<160> 14

<170> PatentIn version 3.0

<210> 1
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<212> DNA
<213> Lactobacillus gasseri

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<221> CDS
<222> (153)..(1946)

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atthaattta ttaaacaccatt ttcaaatcta ttactctcc ccaagcgtaa aatatacgata 120
agagaaaaca ttacttagaaa ggaaaatcat ct atg gaa tct gca cta tat cca 173
Met Glu Ser Ala Leu Tyr Pro
1 5
att caa aat aaa tat cgg ttt aac act tta atg aat ggc act tgg caa 221
Ile Gln Asn Lys Tyr Arg Phe Asn Thr Leu Met Asn Gly Thr Trp Gln
10 15 20
ttt gaa act gat cct aac tct gtt ggt ctt gac gag gga tgg aat aaa 269
Phe Glu Thr Asp Pro Asn Ser Val Gly Leu Asp Glu Gly Trp Asn Lys
25 30 35
gag ttg cct gat cct gaa gaa atg cct gta cca ggt acg ttt gca gaa 317
Glu Leu Pro Asp Pro Glu Glu Met Pro Val Pro Gly Thr Phe Ala Glu
40 45 50 55
tta act act aag cga gac cgt aaa tac tat act gga gac ttt tgg tat 365
Leu Thr Thr Lys Arg Asp Arg Lys Tyr Tyr Thr Gly Asp Phe Trp Tyr
60 65 70
caa aaa gac ttc ttt att cct tca ttt cta aag aag aaa gaa ctt tat 413
Gln Lys Asp Phe Phe Ile Pro Ser Phe Leu Lys Lys Glu Leu Tyr
75 80 85
atc cgt ttt ggt tcg gtt act cat cgc gca aaa gta ttt att aat gga 461
Ile Arg Phe Gly Ser Val Thr His Arg Ala Lys Val Phe Ile Asn Gly
90 95 100
cat gaa gtc ggt caa cat gaa ggt ggt ttt tta cca ttt caa gta aaa 509
His Glu Val Gly Gln His Glu Gly Gly Phe Leu Pro Phe Gln Val Lys

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105	110	115	
att tca aat tat att aat tac gac caa act aat cgt gta act gtt tta Ile Ser Asn Tyr Ile Asn Tyr Asp Gln Thr Asn Arg Val Thr Val Leu 120 125 130 135			557
gtc aat aac gaa tta tct gaa aaa gct att cct tgc ggc acc gaa gaa Val Asn Asn Glu Leu Ser Glu Lys Ala Ile Pro Cys Gly Thr Glu Glu 140 145 150			605
atc tta gat aac ggt caa aaa ctt gct caa cct tat ttt gat ttc ttc Ile Leu Asp Asn Gly Gln Lys Leu Ala Gln Pro Tyr Phe Asp Phe Phe 155 160 165			653
aat tat tct ggc att atg cgg aat gtc tgg ctc tta gca ctt cct caa Asn Tyr Ser Gly Ile Met Arg Asn Val Trp Leu Leu Ala Leu Pro Gln 170 175 180			701
agc caa atc act aat ttt aaa cta aat tat caa tta gca aat aat aag Ser Gln Ile Thr Asn Phe Lys Leu Asn Tyr Gln Leu Ala Asn Asn Lys 185 190 195			749
gca aca att acc tac aat atc gag gca aat aat aat gct gaa ttt aaa Ala Thr Ile Thr Tyr Asn Ile Glu Ala Asn Asn Asn Ala Glu Phe Lys 200 205 210 215			797
gta aca ctt ttc gat aat caa aaa gaa gta gcg tgt gct act tct aaa Val Thr Leu Phe Asp Asn Gln Lys Glu Val Ala Cys Ala Thr Ser Lys 220 225 230			845
aat act agt agt tta aca att aag aat ccg cac ctt tgg agt cca aac Asn Thr Ser Ser Leu Thr Ile Lys Asn Pro His Leu Trp Ser Pro Asn 235 240 245			893
gat ccg tat tca tac aaa ata aag att gaa atg ctc gaa gac gga aaa Asp Pro Tyr Ser Tyr Lys Ile Lys Ile Glu Met Leu Glu Asp Gly Lys 250 255 260			941
aca gtt gac gaa tac aca gat aaa att ggt atc cgc aca gtt aaa att Thr Val Asp Glu Tyr Thr Asp Lys Ile Gly Ile Arg Thr Val Lys Ile 265 270 275			989
gtg aat gat aaa atc ttg ctc aat aat cac cca att tat tta aaa ggc Val Asn Asp Lys Ile Leu Leu Asn Asn His Pro Ile Tyr Leu Lys Gly 280 285 290 295			1037
ttt ggc aag cac gaa gat ttt aat gtt tta ggc aaa gca gtt aac gaa Phe Gly Lys His Glu Asp Phe Asn Val Leu Gly Lys Ala Val Asn Glu 300 305 310			1085
agc att atc aaa cgc gac tac gaa tgc atg aaa tgg att ggc gct aac Ser Ile Ile Lys Arg Asp Tyr Glu Cys Met Lys Trp Ile Gly Ala Asn 315 320 325			1133
tgt ttt aga agc agt cac tat cct tac gcc gaa gaa tgg tat caa tat Cys Phe Arg Ser Ser His Tyr Pro Tyr Ala Glu Glu Trp Tyr Gln Tyr 330 335 340			1181
gcc gat aaa tat ggc ttt tta att att gat gaa gta ccc gct gtt ggt Ala Asp Lys Tyr Gly Phe Leu Ile Ile Asp Glu Val Pro Ala Val Gly 345 350 355			1229
ctt aat cgt tca ata act aac ttt ctt aat gta act aat tct aat cag Leu Asn Arg Ser Ile Thr Asn Phe Leu Asn Val Thr Asn Ser Asn Gln 360 365 370 375			1277

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tcg cac ttt ttt gct tcg aaa act gtg cct gaa tta aaa aag gtc cat Ser His Phe Phe Ala Ser Lys Thr Val Pro Glu Leu Lys Lys Val His 380	385	390	1325
gaa caa gaa ata aaa gaa atg atc gat cgc gac cag cgt cac cct tca Glu Gln Glu Ile Lys Glu Met Ile Asp Arg Asp Gln Arg His Pro Ser 395	400	405	1373
gtg att gcc tgg agt tta ttc aat gaa cca gaa tca act act caa gaa Val Ile Ala Trp Ser Leu Phe Asn Glu Pro Glu Ser Thr Thr Gln Glu 410	415	420	1421
tcc tat gac tat ttc aaa gat att ttt gcc ttt gcg aga aaa ttg gat Ser Tyr Asp Tyr Phe Lys Asp Ile Phe Ala Phe Ala Arg Lys Leu Asp 425	430	435	1469
cca caa aat cgt cct tat act gga act tta gtt atg ggt agc ggt cca Pro Gln Asn Arg Pro Tyr Thr Gly Thr Leu Val Met Gly Ser Gly Pro 440	445	450	1517
aaa gtg gat aag ctt cac cca ctt tgt gac ttt gtc tgc tta aac cgt Lys Val Asp Lys Leu His Pro Leu Cys Asp Phe Val Cys Leu Asn Arg 460	465	470	1565
tat tat ggt tgg tac gtt gct ggt cct gaa atc gtt aat gct aaa Tyr Tyr Gly Trp Tyr Val Ala Gly Gly Pro Glu Ile Val Asn Ala Lys 475	480	485	1613
aag atg ctg gaa gat gaa cta gac ggc tgg caa aac tta aag ctt aat Lys Met Leu Glu Asp Glu Leu Asp Gly Trp Gln Asn Leu Lys Leu Asn 490	495	500	1661
aaa cca ttt gtc ttt act gag ttt ggc gct gat aca tta tct tct tct Lys Pro Phe Val Phe Thr Glu Phe Gly Ala Asp Thr Leu Ser Ser Ser 505	510	515	1709
cat cgc ctt cca gat gaa atg tgg agc caa gaa tat caa aat gaa tat His Arg Leu Pro Asp Glu Met Trp Ser Gln Glu Tyr Gln Asn Glu Tyr 520	525	530	1757
tat caa atg tat ttt gat ata ttt aag aaa tat cca ttt att tgt ggc Tyr Gln Met Tyr Phe Asp Ile Phe Lys Lys Tyr Pro Phe Ile Cys Gly 540	545	550	1805
gaa tta gtt tgg aac ttt gct gac ttt aag acg agt gaa gga atc atg Glu Leu Val Trp Asn Phe Ala Asp Phe Lys Thr Ser Glu Gly Ile Met 555	560	565	1853
cgt gtt ggt ggt aac gat aaa gga att ttt act cgc gat cgt gaa cct Arg Val Gly Gly Asn Asp Lys Gly Ile Phe Thr Arg Asp Arg Glu Pro 570	575	580	1901
aaa gat att gcc ttt acc ttg aaa aag aga tgg caa caa tta aat Lys Asp Ile Ala Phe Thr Leu Lys Lys Arg Trp Gln Gln Leu Asn 585	590	595	1946
taatatttta gttttcacaa ataatcgatgc tcaattaaaa ataatcgata tcatttttagt tcatttgata tcgatttattt gattatggc gcgatttttt attgattttg ataataattt ctaactaaga aatgtttcat taatttatga aactaatatc ttgtttctta aacaaatcat atacaactaa gtctgatgaa tcca			2006
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<210> 2
<211> 598
<212> PRT
<213> Lactobacillus gasseri

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20 25 30

Leu Asp Glu Gly Trp Asn Lys Glu Leu Pro Asp Pro Glu Glu Met Pro
35 40 45

Val Pro Gly Thr Phe Ala Glu Leu Thr Thr Lys Arg Asp Arg Lys Tyr
50 55 60

Tyr Thr Gly Asp Phe Trp Tyr Gln Lys Asp Phe Phe Ile Pro Ser Phe
65 70 75 80

Leu Lys Lys Lys Glu Leu Tyr Ile Arg Phe Gly Ser Val Thr His Arg
85 90 95

Ala Lys Val Phe Ile Asn Gly His Glu Val Gly Gln His Glu Gly Gly
100 105 110

Phe Leu Pro Phe Gln Val Lys Ile Ser Asn Tyr Ile Asn Tyr Asp Gln
115 120 125

Thr Asn Arg Val Thr Val Leu Val Asn Asn Glu Leu Ser Glu Lys Ala
130 135 140

Ile Pro Cys Gly Thr Glu Glu Ile Leu Asp Asn Gly Gln Lys Leu Ala
145 150 155 160

Gln Pro Tyr Phe Asp Phe Asn Tyr Ser Gly Ile Met Arg Asn Val
165 170 175

Trp Leu Leu Ala Leu Pro Gln Ser Gln Ile Thr Asn Phe Lys Leu Asn
180 185 190

Tyr Gln Leu Ala Asn Asn Lys Ala Thr Ile Thr Tyr Asn Ile Glu Ala
195 200 205

Asn Asn Asn Ala Glu Phe Lys Val Thr Leu Phe Asp Asn Gln Lys Glu
210 215 220

Val Ala Cys Ala Thr Ser Lys Asn Thr Ser Ser Leu Thr Ile Lys Asn
225 230 235 240

Pro His Leu Trp Ser Pro Asn Asp Pro Tyr Ser Tyr Lys Ile Lys Ile
245 250 255

Glu Met Leu Glu Asp Gly Lys Thr Val Asp Glu Tyr Thr Asp Lys Ile
260 265 270

Gly Ile Arg Thr Val Lys Ile Val Asn Asp Lys Ile Leu Leu Asn Asn
275 280 285

His Pro Ile Tyr Leu Lys Gly Phe Gly Lys His Glu Asp Phe Asn Val
290 295 300

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Leu Gly Lys Ala Val Asn Glu Ser Ile Ile Lys Arg Asp Tyr Glu Cys
305 310 315 320

Met Lys Trp Ile Gly Ala Asn Cys Phe Arg Ser Ser His Tyr Pro Tyr
325 330 335

Ala Glu Glu Trp Tyr Gln Tyr Ala Asp Lys Tyr Gly Phe Leu Ile Ile
340 345 350

Asp Glu Val Pro Ala Val Gly Leu Asn Arg Ser Ile Thr Asn Phe Leu
355 360 365

Asn Val Thr Asn Ser Asn Gln Ser His Phe Phe Ala Ser Lys Thr Val
370 375 380

Pro Glu Leu Lys Lys Val His Glu Gln Glu Ile Lys Glu Met Ile Asp
385 390 395 400

Arg Asp Gln Arg His Pro Ser Val Ile Ala Trp Ser Leu Phe Asn Glu
405 410 415

Pro Glu Ser Thr Thr Gln Glu Ser Tyr Asp Tyr Phe Lys Asp Ile Phe
420 425 430

Ala Phe Ala Arg Lys Leu Asp Pro Gln Asn Arg Pro Tyr Thr Gly Thr
435 440 445

Leu Val Met Gly Ser Gly Pro Lys Val Asp Lys Leu His Pro Leu Cys
450 455 460

Asp Phe Val Cys Leu Asn Arg Tyr Tyr Gly Trp Tyr Val Ala Gly Gly
465 470 475 480

Pro Glu Ile Val Asn Ala Lys Lys Met Leu Glu Asp Glu Leu Asp Gly
485 490 495

Trp Gln Asn Leu Lys Leu Asn Lys Pro Phe Val Phe Thr Glu Phe Gly
500 505 510

Ala Asp Thr Leu Ser Ser His Arg Leu Pro Asp Glu Met Trp Ser
515 520 525

Gln Glu Tyr Gln Asn Glu Tyr Tyr Gln Met Tyr Phe Asp Ile Phe Lys
530 535 540

Lys Tyr Pro Phe Ile Cys Gly Glu Leu Val Trp Asn Phe Ala Asp Phe
545 550 555 560

Lys Thr Ser Glu Gly Ile Met Arg Val Gly Gly Asn Asp Lys Gly Ile
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Arg Trp Gln Gln Leu Asn
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<210> 3
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<223> Synthetic Oligonucleotide Primer.

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<210> 11
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<222> (1)..(30)
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<400> 12
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